

BEST AVAILABLE COPY

SEP. 6. 2006 2:58PM

RMS Patent Department

NO. 125 P. 15

Application No. 09/823,649

Appendix D
(6 pages)

ExPASy Home page Site Map Search [Swiss-Prot/TrEMBL] for []

Contact us Swiss-Prot

Print friendly view Print friendly version Print friendly search Print history

UniProtKB/Swiss-Prot entry O52225

*Swiss-Prot

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence]

[Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	DPO1_THEFI
Primary accession number	O52225
Secondary accession numbers	None
Integrated into Swiss-Prot on	December 15, 1998
Sequence was last modified on	June 1, 1998 (Sequence version 1)
Annotations were last modified on	March 7, 2006 (Entry version 38)
Name and origin of the protein	DNA polymerase I, thermostable
Protein name	EC 2.7.7.7
Synonyms	TFI polymerase 1
Gene name	Name: polA Synonyms: pol
From	Thermus filiformis [TaxID: 276]
Taxonomy	Bacteria: Deinococcus-Thermus: Deinococci: Thermoales: Thermaceae: Thermus.
References	

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

PubMed=9509419 [NCBI], ExPASY, EBI, Israel, Japan]

Jung S.E., Choi J.J., Kim H.K., Kwon S.-T.;

"Cloning and analysis of the DNA polymerase-encoding gene from *Thermus filiformis*.",
Mol. Cells 7:769-776(1997).**Comments**

- **FUNCTION:** Has 5'-to-3' exonuclease activity and no 3'-to-5' exonuclease activity.
- **CATALYTIC ACTIVITY:** Deoxynucleoside triphosphate + DNA(n) = diphosphate + DNA(n+1).
- **BIOPHYSICOCHEMICAL PROPERTIES:**
 - **Temperature dependence:** Thermostable;
 - **SIMILARITY:** Belongs to the DNA polymerase type-A family.
 - **SIMILARITY:** Contains 1 5'-3' exonuclease domain.

CopyrightCopyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.**Cross-references****Sequence databases**

EMBL AF030320; AAC46079.1; ; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databasesHSSP P19821; 1TAQ [HSSP ENTRY / PDB]
ModBase O52225.**Protein-protein interaction databases**DIP O52225.
2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Family and domain databasesIPR002421; 5_3'_exonuclease.
IPR001098; DNA_pol.
IPR002298; DNA_pol.
IPR000513; Exo_N_I.
InterPro

PR008918; HhH2.
 PR012337; RNaseH_fold.
 Graphical view of domain structure.
 PF01367; 5_3_exonuc; 1.
 PF02739; 5_3_exonuc_N; 1.
 PF00476; DNA_pol_A; 1.
 Pfam graphical view of domain structure.

Pfam

PRINTS PR00868; DNAPOLI.
 SM00475; 53EXOc; 1.
 SM00279; HhH2; 1.
 SM00482; POLAc; 1.
 SMART graphical view of domain structure.

TIGRFAMs TIGR00593; polA; 1.
 PROSITE PS00447; DNA_POLYMERASE_A; 1.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 BLOCKS 052225.

Other

ProtoNet 052225.

UniRef

View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

DNA_damage; DNA_repair; DNA_replication; DNA-binding; DNA-directed_DNA_polymerase; Nucleotidyltransferase;
 Transferase.

Features

Key	From	To	Length	Description	FID
CHAIN	1	833	833	DNA polymerase I, thermostable.	PRO_0000101260
REGION	412	833	422	Polymerase (By similarity).	

Sequence information

Length: 833 AA [This is the length of the unprocessed precursor]
 Molecular weight: 93891 Da [This is the MW of the unprocessed precursor]
 CRC64: 51BF8B0417EEFC4D [This is a checksum on the sequence]

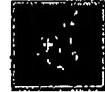
10	20	30	40	50	60
MTPFLFDLLEEP	PKRVLLVDGH	HAYRTTFYAL	SLTTSRGEPV	QMVYGRARSIL	LKALKEDGQA
70	80	90	100	110	120
VVVVFDAKAP	SFRHEAYEAY	KAGRPTPED	FPRQLALYKR	LVDLLGLVRL	EAPGYEADDV
130	140	150	160	170	180
LGTFLAKKAER	EGMEVRILTG	DRDFFQLLSE	KVSVLLPDGT	LVTPKDVQEK	YGVPPERWVD
190	200	210	220	230	240
FRALTGDRSD	NIPGVAGIGE	KTALRLLAEW	GSEVNLLKNL	DRVKPDSLRR	KIEAHLEDLH
250	260	270	280	290	300
LSDLDLARIRT	DLPLEVDEKA	LRRRTPDLEG	LRAFLEELF	GSSLHFGLL	GGEKPREEAP
310	320	330	340	350	360
WPPEGAFVG	FLLSRKEPMW	AELLALAAS	EGRVHRATSP	VEALADLKEA	RGFLAKDLAV
370	380	390	400	410	420
LALREGVALD	PTDDPLLVAY	LIDPANTHPE	GVARRYGEF	TEDAAERALL	SERLFQNLFP
430	440	450	460	470	480
RNSEKLLMLY	QEVERTPLSRV	LAHMEARGVR	LDVPLILEALS	FELEKEMERL	EGEVFRLAGH
490	500	510	520	530	540
PFNLNNSRDQL	ERVLFDDELGL	TPVGRTTEKTG	KRSTAQGALE	ALRGAHPIVE	LILQYRELSK
550	560	570	580	590	600
LKSTYLDPLP	RLVHPRTGRL	HTRENQTATA	TGRLLSSDPN	LQNI PVRTPL	GQRIRKAFVA
610	620	630	640	650	660
EEGMILLAAAD	YSQTELRVLA	HLSGDENCNRKR	VEREGKDIHT	ETAAMMFGILD	PALVDPKMRR
670	680	690	700	710	720

AAKTVNFGVL YGMSAHLRSQ ELGIDYKEAE AFIERYFQSF PKVRAWIERT LEEGRTRGYV
730 740 750 760 770 780
ETLFGRRRVV PDLASRVRSV REAAERMAFN MPVQGTAADL MKLAMVKLFP RLKPLGAHLL
790 800 810 820 830
LQVHDELVLE VPEDRAEAK ALVKEVMENA YPLDVPLEVE VGYGRDWLEA KQD

O52225 in FASTA format

[View entry in original UniProtKB/Swiss-Prot format](#)[View entry in raw text format \(no links\)](#)[Report form for errors/updates in this UniProtKB/Swiss-Prot entry](#)**BLAST** BLAST submission on ExPASy/SIB or at NCB (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

**ScanProsite, MotifScan****NPSA** NPSA Sequence analysis tools[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)

Hosted by SIB Switzerland Mirror sites: Australia Brazil Canada China Korea

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Search Swiss-Prot/TREMBL](#) for

Feature aligner

Selected features of Q52225 (DPO1_THEF) DNA polymerase I, thermostable (EC 2.7.7.7) (TFI polymerase 1) [Thermus filiformis].

REGION 412-833 422 Polymerase (By similarity)

Key	Position	Length	Description
<input type="checkbox"/> CHAIN	1-833	833	DNA polymerase I, thermostable
MTPLEFDLDEEP PKRVLLDVGH HLYAIRTFFYAL SUTTSRGEPV QMVYGFARS L LKALKEDQQA WIVVYFDAKAP SFRHEAYEAY KAGRAGPTPED FPRQLALVKR LYDLIGLGLWRL EAPGYEADDV LGTLAKKAER EGMYVRILTG DRDFEQQLSSE FVSVLLPDGT LYTPKTDYQEK YGVPPPERMWD FRALTGDRSD NLPGVAGTCIE KTAFLRLLAEW GSEVENLLKL DRVKDPSLRR KLFEAHLFEDIH LSUDLARIIT DPLIEVDKFA LRREPTDLEG LRAFLLEELF GSLLHEFGLL GGEKPREEAP WPPPEGAFVG FLLSRKEPMW AEILALAAS ECRVHRAITSP VRALADLKEA RGPLAKDLYV LALREGVALD PTDDPLLYAV LLDPANTHPE GVARRYGGEF TDEAAE2ALL SBRLLFQNLFP RLSEKLLWLY QEVERTPLSRV LAHMBAARGUR LDVPLLEALS FELEKEMERL EGEVPRLAGH PFMNLSRDQL ERVLFDDELGL TPVGRTTEKTG KRSTAGQGALB ALRGAHPIVE LILQYRELISK LKSSTYLDLPL RLVHPRTGRL HTRFNQDTAA TGRLSSSDPN IONLIPVTPPL GQRIRKAPVA EGGWLLAAD YSQIELEVLA HLSGDENLKR VFREGKDHT ETAAMNGFLD PALVDEKMRV AAKTVNPGVL YMGSAAHRSQ ELGIDYKEAE AFIERYFQSF PKVRAWIERT LREGRTRGYV STLGFRRRYYV PDLASRVSRSV REAAERMAFN MPVQGTAAIDL MKIAMVKLFP RLKPLGAHLL LQVHDELVLE VPEDRAEAKA ALVKEVMENA YPLDVPLEVE VGVRGDWLEA KQD			

REGION 412-833 422 Polymerase (By similarity)

ERLFONLFFP LSEKKLLMLYQ EVERPLPSRYVL AHMEARGVRL DVPLLEALSF ELEKEMERLE GEVFRLAGHP
FNLNSRDQLE RVLFDDELGLT PVGRTEKTGK RSTAOGALEA LRGAHPIVEL ILCYRETSKL KSTYLDPLPR
LHVHPRTGRLH TRPNQTATAT GRILSSSDPNL QNIPVTPPLG QRIRKAVAE EGWLILLAADY SQIELRVLAH
LSGDENLKRV FREGKDIHTE TAAWMFCGLDP ALVDPKMRRRA AKTVNPGVLY GMSAHRISQE LGIDYKEAEA
PIERYFQSFV KVRAWIERTL EGRTRTRGYVE TLFGRRRYVP DLASRVSRSV EAERMAFN PVQGTAADLM
KIAMVKLFFR LKPLGAHLL QVHDELVLYV PEDRAEAKA LVKEVMENAY PLDVPLVEVEV GVGRDWLEAK QD

[Align with Swiss-Prot](#) [Align with TREMBL](#) [Align with ExPASy](#) [Align with Swiss-Prot/TREMBL](#)

[ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Swiss-Prot](#) [Proteomics tools](#)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER: _____**

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.